Claims

1. A protein, characterised in that it displays the amino acid sequence represented in SEQ ID NO:4.

2. A protein that is a homologue of the protein according to claim 1 and which displays an amino acid sequence homologous to the sequence represented in SEQ ID NO:4, wherein the protein displays arginine at position 303 and lysine at position 311.

3. The protein according to claim 2, which displays a degree of homology of at least 95%.

4. The protein according to claim 3, which displays a degree of homology of at least 97%.

5. The protein according to claim 3 or 4, which displays a degree of homology of at least 99%.

6. A peptide, characterised in that it is a fragment of the protein according to claims 1 to 5 and displays an amino acid sequence that contains the sequence region that includes the amino acid positions 303 and 311 in SEQ ID NO:4.

7. The peptide according to claim 6, characterised in that it displays a length of 53 to 315 amino acids.

8. A nucleic acid, characterised in that it encodes a protein or a peptide according to claims 1 to 7.

9. The nucleic acid according to claim 8, characterised in that it displays the nucleic acid sequence represented in SEQ ID NO:3.

10. The nucleic acid according to claim 8, characterised in that it displays a nucleic acid sequence that contains the sequence region that includes the nucleic acid positions 979-981 and 1003-1005 in SEQ ID NO:3.

11. An antibody that is directed against a protein or peptide according to claims 1 to 7.

12. The antibody according to claim 11, characterised in that it is a monoclonal or polyclonal antibody.

13. A method to determine the tendency of falling ill with type 1 diabetes, wherein genomic DNA is amplified from isolated mononuclear blood cells, and sequenced, and where modifications of or deviations from the nucleic acid sequence are determined, this sequence coding for a protein with the amino acid sequence represented in SEQ ID NO:6, where deviations of codons (non-silent mutations) display increased tendency for falling ill with an autoimmune disease, type 2 diabetes, cancer or disruptions to the mineral and lipoid metabolism.

14. The method according to claim 13, wherein for amplification the following primers are used: K815-F/K817-R; K815-F/K875; K821-F/K817-R; K821-F/K870-R; K874-F/K870-R; K823-F/K825-R; K884-F/K806-R; K801-F/K804-R; K814-F/KK832-R; K828-F/K833-R; K831-F/K817-R; K815-F/K870-R; K815-F/K818-R; K816-F/K819-R; K834-F/K836-R, F15/R12; F15/R14; F15/R13; F57/R16; F57/R20; F57/R21; F59/RR25;

F59/RR30; F59/R33; F95/RR34; F96/R39; F95/R48; F95/R50; F60/R7; F60/R8; F60/R66; F60/R67; F96/R76; F96/R77; F96/R81 F96/R83; F33/R1; F33/R4; F33/R15; F39/R28; F40/R3; or F41/R5.

15. A method to determine the tendency of falling ill with type 1 diabetes, wherein RNA is isolated from isolated mononuclear blood cells or tissue biopsies, amplified and quantified, where enhanced/reduced expression indicates an increased/reduced tendency to fall ill with type 1 diabetes, autoimmune diseases in general, type 2 diabetes, cancer or disruptions to the mineral and lipoid metabolism.

16. Use of a protein or peptide according to claims 1 to 7 for the manufacture of a pharmaceutical compound.

17. Use of a nucleic acid according to claims 8 to 10 or of an antisense oligonucleotide of the same for the manufacture of a pharmaceutical compound.

18. A pharmaceutical composition that contains a nucleic acid according to claims 8 to 10, or an antisense oligonucleotide of the same.

19. A pharmaceutical composition that contains a protein and/or a peptide according to claims 1 to 7.

20. The composition according to claim 18 or 19, characterised in that it also contains pharmaceutically compatible excipients and/or carriers.

21. The composition according to claims 18 to 20, characterised in that the compound is formulated for intravenous application.

22. A transgenic non-human mammal, wherein the germ and somatic cells contain a nucleic acid or a nucleic acid segment which encodes a protein with the amino acid sequence shown in SEQ ID NO:2 or an amino acid sequence homologous to that, with a degree of homology of at least 95%, preferably at least 97%, and most preferably 99%, and where the homologous amino acid sequence displays methionine at position 303 and arginine at position 311.

23. The transgenic mammal according to claim 22, characterised in that it expresses the protein in the pancreas.

24. The mammal according to claim 22 or 23, characterised in that it is a rat.

25. Use of a transgenic or congenic non-human mammal, whose gamete and somatic cells contain a nucleic acid or a nucleic acid segment which encodes a protein with the amino acid sequence shown in SEQ ID NO:2 or an amino acid sequence homologous to that, with a degree of homology of at least 95%, preferably at least 97%, and most preferably 99%, and where the homologous amino acid sequence displays methionine at position 303 and arginine at position 311, for the purpose of identifying diabetes protective substances.

26. The use according to claim 25, wherein the degree of homology is at least 97%.

27. The use according to claim 25 or 26, wherein the degree of homology is at least 99%.

28. A kit for performing a method according to claims 13 to 15.